

SEQUENCE LISTING

<110> BASF Plant Science GmbH
SweTree Technologies AB

5

<120> IMPROVED CONSTRUCTS FOR MARKER EXCISION BASED ON DUAL-FUNCTION
SELECTION MARKER

10 <130> PF 55443 EP

<160> 16

<170> PatentIn version 3.1

15

$\langle 210 \rangle$ 1

<211> 1160

<212> DNA

<213> Rhodosporidium toruloides

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 $\langle 220 \rangle$

<221> CDS

<222> (1) .. (1104)

<223> coding for DAAO

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Met His Ser Gln Lys Arg Val Val Val Leu Gly Ser Gly Val Ile Gly

1 5 10 15

30

ctg agc agc gcc ctc atc ctc gct cgg aag ggc tac agc gtg cat att 96

Leu Ser Ser Ala Leu Ile Leu Ala Arg Lys Gly Tyr Ser Val His Ile

20 25 30

35 ctc gcg cgc gac ttg ccg gag gac gtc tcg agc caa act ttc gct tca 144

Leu Ala Arg Asp Leu Pro Glu Asp Val Ser Ser Gln Thr Phe Ala Ser

35 40 45

cca tgg gct ggc gcg aat tgg acg cct ttc atg acg ctt aca gac ggt 192

cca tgg gct ggc gcg aat tgg acg cct ttc atg acg ctt aca gac ggt
Pro Trp Ala Gly Ala Asn Trp Thr Pro Phe Met Thr Leu Thr Asp Gl

50 55 60

cct cga caa gca aaa tgg gaa gaa tcg act ttc aag aag tgg gtc gag 240

cct cga caa gca aaa tgg gaa gaa tcg act ttc aag aag tgg gtc gag
Pro Arg Gln Ala Lys Trp Glu Glu Ser Thr Phe Lys Lys Trp Val Glu

45 65 70 75 80

	ttg gtc ccg acg ggc cat gcc atg tgg ctc aag ggg acg agg cgg ttc	288
	Leu Val Pro Thr Gly His Ala Met Trp Leu Lys Gly Thr Arg Arg Phe	
	85 90 95	
5	gcg cag aac gaa gac ggc ttg ctc ggg cac tgg tac aag gac atc acg	336
	Ala Gln Asn Glu Asp Gly Leu Leu Gly His Trp Tyr Lys Asp Ile Thr	
	100 105 110	
10	cca aat tac cgc ccc ctc cca tct tcc gaa tgt cca cct ggc gct atc	384
	Pro Asn Tyr Arg Pro Leu Pro Ser Ser Glu Cys Pro Pro Gly Ala Ile	
	115 120 125	
15	ggc gta acc tac gac acc ctc tcc gtc cac gca cca aag tac tgc cag	432
	Gly Val Thr Tyr Asp Thr Leu Ser Val His Ala Pro Lys Tyr Cys Gln	
	130 135 140	
20	tac ctt gca aga gag ctg cag aag ctc ggc gcg acg ttt gag aga cgg	480
	Tyr Leu Ala Arg Glu Leu Gln Lys Leu Gly Ala Thr Phe Glu Arg Arg	
	145 150 155 160	
25	acc gtt acg tcg ctt gag cag gcg ttc gac ggt gcg gat ttg gtg gtc	528
	Thr Val Thr Ser Leu Glu Gln Ala Phe Asp Gly Ala Asp Leu Val Val	
	165 170 175	
30	aac gct acg gga ctt ggc gcc aag tcg att gcg ggc atc gac gac caa	576
	Asn Ala Thr Gly Leu Gly Ala Lys Ser Ile Ala Gly Ile Asp Asp Gln	
	180 185 190	
35	gcc gcc gag cca atc cgc ggg caa acc gtc ctc gtc aag tcc cca tgc	624
	Ala Ala Glu Pro Ile Arg Gly Gln Thr Val Leu Val Lys Ser Pro Cys	
	195 200 205	
40	aag cga tgc acg atg gac tcg tcc gac ccc gct tct ccc gcc tac atc	672
	Lys Arg Cys Thr Met Asp Ser Ser Asp Pro Ala Ser Pro Ala Tyr Ile	
	210 215 220	
45	att ccc cga cca ggt ggc gaa gtc atc tgc ggc ggg acg tac ggc gtg	720
	Ile Pro Arg Pro Gly Gly Glu Val Ile Cys Gly Gly Thr Tyr Gly Val	
	225 230 235 240	
50	gga gac tgg gac ttg tct gtc aac cca gag acg gtc cag cgg atc ctc	768
	Gly Asp Trp Asp Leu Ser Val Asn Pro Glu Thr Val Gln Arg Ile Leu	
	245 250 255	

aag cac tgc ttg cgc ctc gac ccg acc atc tcg agc gac gga acg atc 816
 Lys His Cys Leu Arg Leu Asp Pro Thr Ile Ser Ser Asp Gly Thr Ile
 260 265 270

5 gaa ggc atc gag gtc ctc cgc cac aac gtc ggc ttg cga cct gca cga 864
 Glu Gly Ile Glu Val Leu Arg His Asn Val Gly Leu Arg Pro Ala Arg
 275 280 285

10 cga ggc gga ccc cgc gtt gag gca gaa cgg atc gtc ctg cct ctc gac 912
 Arg Gly Gly Pro Arg Val Glu Ala Glu Arg Ile Val Leu Pro Leu Asp
 290 295 300

15 cgg aca aag tcg ccc ctc tcg ctc ggc agg ggc agc gca cga gcg gcg 960
 Arg Thr Lys Ser Pro Leu Ser Leu Gly Arg Gly Ser Ala Arg Ala Ala
 305 310 315 320

20 aag gag aag gag gtc acg ctt gtg cat gcg tat ggc ttc tcg agt gcg 1008
 Lys Glu Lys Glu Val Thr Leu Val His Ala Tyr Gly Phe Ser Ser Ala
 325 330 335

gga tac cag cag agt tgg ggc gcg gcg gag gat gtc gcg cag ctc gtc 1056
 Gly Tyr Gln Gln Ser Trp Gly Ala Ala Glu Asp Val Ala Gln Leu Val
 340 345 350

25 gac gag gcg ttc cag cgg tac cac ggc gcg gcg cgg gag tcg aag ttg 1104
 Asp Glu Ala Phe Gln Arg Tyr His Gly Ala Ala Arg Glu Ser Lys Leu
 355 360 365

30 tagggcgggga tttgtggctg tattgcgggc atctacaaga aaaaaaaaaa aaaaaa 1160

<210> 2
 <211> 368
 <212> PRT
 35 <213> Rhodosporidium toruloides

<400> 2
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40 Leu Ser Ser Ala Leu Ile Leu Ala Arg Lys Gly Tyr Ser Val His Ile
 20 25 30

45 Leu Ala Arg Asp Leu Pro Glu Asp Val Ser Ser Gln Thr Phe Ala Ser
 35 40 45

Pro Trp Ala Gly Ala Asn Trp Thr Pro Phe Met Thr Leu Thr Asp Gly
 50 55 60

5 Pro Arg Gln Ala Lys Trp Glu Glu Ser Thr Phe Lys Lys Trp Val Glu
 65 70 75 80

Leu Val Pro Thr Gly His Ala Met Trp Leu Lys Gly Thr Arg Arg Phe
 85 90 95

10 Ala Gln Asn Glu Asp Gly Leu Leu Gly His Trp Tyr Lys Asp Ile Thr
 100 105 110

Pro Asn Tyr Arg Pro Leu Pro Ser Ser Glu Cys Pro Pro Gly Ala Ile
 115 120 125

Gly Val Thr Tyr Asp Thr Leu Ser Val His Ala Pro Lys Tyr Cys Gln
 130 135 140

20 Tyr Leu Ala Arg Glu Leu Gln Lys Leu Gly Ala Thr Phe Glu Arg Arg
 145 150 155 160

Thr Val Thr Ser Leu Glu Gln Ala Phe Asp Gly Ala Asp Leu Val Val
 165 170 175

25 Asn Ala Thr Gly Leu Gly Ala Lys Ser Ile Ala Gly Ile Asp Asp Gln
 180 185 190

Ala Ala Glu Pro Ile Arg Gly Gln Thr Val Leu Val Lys Ser Pro Cys
 195 200 205

Lys Arg Cys Thr Met Asp Ser Ser Asp Pro Ala Ser Pro Ala Tyr Ile
 210 215 220

35 Ile Pro Arg Pro Gly Gly Glu Val Ile Cys Gly Gly Thr Tyr Gly Val
 225 230 235 240

Gly Asp Trp Asp Leu Ser Val Asn Pro Glu Thr Val Gln Arg Ile Leu
 245 250 255

40 Lys His Cys Leu Arg Leu Asp Pro Thr Ile Ser Ser Asp Gly Thr Ile
 260 265 270

Glu Gly Ile Glu Val Leu Arg His Asn Val Gly Leu Arg Pro Ala Arg
 275 280 285

45

Arg Gly Gly Pro Arg Val Glu Ala Glu Arg Ile Val Leu Pro Leu Asp
 290 295 300

5 Arg Thr Lys Ser Pro Leu Ser Leu Gly Arg Gly Ser Ala Arg Ala Ala
 305 310 315 320

Lys Glu Lys Glu Val Thr Leu Val His Ala Tyr Gly Phe Ser Ser Ala
 325 330 335

10 Gly Tyr Gln Gln Ser Trp Gly Ala Ala Glu Asp Val Ala Gln Leu Val
 340 345 350

15 Asp Glu Ala Phe Gln Arg Tyr His Gly Ala Ala Arg Glu Ser Lys Leu
 355 360 365

<210> 3
 <211> 1005
 <212> DNA
 20 <213> *Caenorhabditis elegans*

<220>
 <221> CDS
 <222> (1)..(1002)
 25 <223> coding for DAAO

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 Met Ala Asn Ile Ile Pro Lys Ile Ala Ile Ile Gly Glu Gly Val Ile
 30 1 5 10 15

gga tgt act tca gca ctt caa ata tca aaa gct ata cca aat gcg aaa 96
 Gly Cys Thr Ser Ala Leu Gln Ile Ser Lys Ala Ile Pro Asn Ala Lys
 20 25 30

35 ata act gtg ctc cac gat aaa cca ttt aaa aaa tcg tgc agt gca gga 144
 Ile Thr Val Leu His Asp Lys Pro Phe Lys Lys Ser Cys Ser Ala Gly
 35 40 45

40 cca gca gga tta ttt aga atc gat tat gag gag aat act gaa tac gga 192
 Pro Ala Gly Leu Phe Arg Ile Asp Tyr Glu Glu Asn Thr Glu Tyr Gly
 50 55 60

cgt gct tct ttc gcc tgg ttc tca cat ctc tat cgc act aca aaa gga 240
 45 Arg Ala Ser Phe Ala Trp Phe Ser His Leu Tyr Arg Thr Thr Lys Gly

	65	70	75	80	
	tcc gaa acc ggc gtg aaa tta gtt tct gga cat att caa tcc gac aac				288
	Ser Glu Thr Gly Val Lys Leu Val Ser Gly His Ile Gln Ser Asp Asn				
5		85	90	95	
	ttg gag tca ttg aag caa caa caa aga gcc tat ggc gat att gtg tac				336
	Leu Glu Ser Leu Lys Gln Gln Gln Arg Ala Tyr Gly Asp Ile Val Tyr				
10		100	105	110	
	aac ttt aga ttc ttg gat gat aga gaa cgg ctg gac att ttt ccc gaa				384
	Asn Phe Arg Phe Leu Asp Asp Arg Glu Arg Leu Asp Ile Phe Pro Glu				
		115	120	125	
15	cca tca aag cac tgc att cac tac acc gcc tac gca tca gaa ggt aac				432
	Pro Ser Lys His Cys Ile His Tyr Thr Ala Tyr Ala Ser Glu Gly Asn				
		130	135	140	
	aag tac gtg cct tat ttg aag aat ttg ctg ctt gag caa aaa atc gag				480
20	Lys Tyr Val Pro Tyr Leu Lys Asn Leu Leu Leu Glu Gln Lys Ile Glu				
		145	150	155	160
	ttc aag caa caa gaa gtg acg agt ttg gac gca gtc gcc gac gct ggt				528
	Phe Lys Gln Gln Glu Val Thr Ser Leu Asp Ala Val Ala Asp Ala Gly				
25		165	170	175	
	tac gat gtt att gta aac tgc gca ggc ttg tac ggt gga aag ttg gct				576
	Tyr Asp Val Ile Val Asn Cys Ala Gly Leu Tyr Gly Gly Lys Leu Ala				
30		180	185	190	
	ggt gat gac gat act tgc tac ccc att aga gga gtc att ttg gaa gtt				624
	Gly Asp Asp Asp Thr Cys Tyr Pro Ile Arg Gly Val Ile Leu Glu Val				
		195	200	205	
35	gat gca cca tgg cac aag cac ttc aat tat cga gac ttt act act ttc				672
	Asp Ala Pro Trp His Lys His Phe Asn Tyr Arg Asp Phe Thr Thr Phe				
		210	215	220	
	aca att cca aaa gag cac agc gtg gtg gtt ggg tcc acc aag cag gac				720
40	Thr Ile Pro Lys Glu His Ser Val Val Val Gly Ser Thr Lys Gln Asp				
		225	230	235	240
	aat cga tgg gat ttg gag atc acc gac gag gat aga aat gat att ttg				768
	Asn Arg Trp Asp Leu Glu Ile Thr Asp Glu Asp Arg Asn Asp Ile Leu				
45		245	250	255	

aaa cga tac att gct tta cat cct gga atg aga gag cca aag att atc 816
 Lys Arg Tyr Ile Ala Leu His Pro Gly Met Arg Glu Pro Lys Ile Ile
 260 265 270

5
 aaa gaa tgg tca gca ctt cgc ccg gga cgt aag cat gtc aga att gaa 864
 Lys Glu Trp Ser Ala Leu Arg Pro Gly Arg Lys His Val Arg Ile Glu
 275 280 285

10
 gcg cag aag agg aca tct gtt gga aac tca aaa gat tat atg gtt gtg 912
 Ala Gln Lys Arg Thr Ser Val Gly Asn Ser Lys Asp Tyr Met Val Val
 290 295 300

15
 cat cac tat ggt cac ggg agc aac gga ttc acg ttg ggt tgg gga aca 960
 His His Tyr Gly His Gly Ser Asn Gly Phe Thr Leu Gly Trp Gly Thr
 305 310 315 320

20
 gca att gaa gca act aaa ctt gtt aag act gca cta gga tta taa 1005
 Ala Ile Glu Ala Thr Lys Leu Val Lys Thr Ala Leu Gly Leu
 325 330

<210> 4
 <211> 334
 <212> PRT

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 <213> *Caenorhabditis elegans*

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 Gly Cys Thr Ser Ala Leu Gln Ile Ser Lys Ala Ile Pro Asn Ala Lys
 20 25 30

35
 Ile Thr Val Leu His Asp Lys Pro Phe Lys Lys Ser Cys Ser Ala Gly
 35 40 45

Pro Ala Gly Leu Phe Arg Ile Asp Tyr Glu Glu Asn Thr Glu Tyr Gly
 50 55 60

40
 Arg Ala Ser Phe Ala Trp Phe Ser His Leu Tyr Arg Thr Thr Lys Gly
 65 70 75 80

Ser Glu Thr Gly Val Lys Leu Val Ser Gly His Ile Gln Ser Asp Asn
 85 90 95

45

Leu Glu Ser Leu Lys Gln Gln Gln Arg Ala Tyr Gly Asp Ile Val Tyr
 100 105 110

5 Asn Phe Arg Phe Leu Asp Asp Arg Glu Arg Leu Asp Ile Phe Pro Glu
 115 120 125

Pro Ser Lys His Cys Ile His Tyr Thr Ala Tyr Ala Ser Glu Gly Asn
 130 135 140

10 Lys Tyr Val Pro Tyr Leu Lys Asn Leu Leu Leu Glu Gln Lys Ile Glu
 145 150 155 160

Phe Lys Gln Gln Glu Val Thr Ser Leu Asp Ala Val Ala Asp Ala Gly
 165 170 175

15 Tyr Asp Val Ile Val Asn Cys Ala Gly Leu Tyr Gly Gly Lys Leu Ala
 180 185 190

Gly Asp Asp Asp Thr Cys Tyr Pro Ile Arg Gly Val Ile Leu Glu Val
 20 195 200 205

Asp Ala Pro Trp His Lys His Phe Asn Tyr Arg Asp Phe Thr Thr Phe
 210 215 220

25 Thr Ile Pro Lys Glu His Ser Val Val Val Gly Ser Thr Lys Gln Asp
 225 230 235 240

Asn Arg Trp Asp Leu Glu Ile Thr Asp Glu Asp Arg Asn Asp Ile Leu
 245 250 255

30 Lys Arg Tyr Ile Ala Leu His Pro Gly Met Arg Glu Pro Lys Ile Ile
 260 265 270

Lys Glu Trp Ser Ala Leu Arg Pro Gly Arg Lys His Val Arg Ile Glu
 35 275 280 285

Ala Gln Lys Arg Thr Ser Val Gly Asn Ser Lys Asp Tyr Met Val Val
 290 295 300

40 His His Tyr Gly His Gly Ser Asn Gly Phe Thr Leu Gly Trp Gly Thr
 305 310 315 320

Ala Ile Glu Ala Thr Lys Leu Val Lys Thr Ala Leu Gly Leu
 325 330

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<210> 5
 <211> 1186
 <212> DNA
 <213> Nectria haematococca

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<220>
 <221> CDS
 <222> (42)..(1124)
 <223> coding for DAAO

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 Met Ser Asn Thr Ile
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gtc gtc gtt ggt gcc ggt gtc att ggc ttg acg tgc gcc ttg ttg ctc 104
 Val Val Val Gly Ala Gly Val Ile Gly Leu Thr Ser Ala Leu Leu Leu
 10 15 20

20

tcc aag aac aag ggc aac aag atc acc gtc gtg gcc aag cac atg ccc 152
 Ser Lys Asn Lys Gly Asn Lys Ile Thr Val Val Ala Lys His Met Pro
 25 30 35

25

ggc gac tat gac gtt gaa tac gcc tgc cct ttt gct ggt gcc aac cac 200
 Gly Asp Tyr Asp Val Glu Tyr Ala Ser Pro Phe Ala Gly Ala Asn His
 40 45 50

30

tcc ccc atg gcg acg gaa gag agc agc gaa tgg gaa cgt cgc act tgg 248
 Ser Pro Met Ala Thr Glu Glu Ser Ser Glu Trp Glu Arg Arg Thr Trp
 55 60 65

35

tac gag ttt aag aga ctg gtc gag gag gtc cct gag gcc ggt gtt cat 296
 Tyr Glu Phe Lys Arg Leu Val Glu Glu Val Pro Glu Ala Gly Val His
 70 75 80 85

ttc cag aag tct cgc atc cag agg cgc aat gtg gac act gaa aag gcg 344
 Phe Gln Lys Ser Arg Ile Gln Arg Arg Asn Val Asp Thr Glu Lys Ala
 90 95 100

40

cag agg tct ggt ttc cca gac gcc ctc ttc tgc aaa gaa ccc tgg ttc 392
 Gln Arg Ser Gly Phe Pro Asp Ala Leu Phe Ser Lys Glu Pro Trp Phe
 105 110 115

45

aag aac atg ttt gag gac ttc cgt gag cag cac cct agc gag gtc atc 440
 Lys Asn Met Phe Glu Asp Phe Arg Glu Gln His Pro Ser Glu Val Ile

	120	125	130	
	ccc ggt tac gac tct ggc tgc gag ttc aca tcg gtg tgc atc aac acg			488
	Pro Gly Tyr Asp Ser Gly Cys Glu Phe Thr Ser Val Cys Ile Asn Thr			
5	135	140	145	
	gcc atc tac ctc ccc tgg ctc ctc ggc cag tgc atc aag aat ggc gtc			536
	Ala Ile Tyr Leu Pro Trp Leu Leu Gly Gln Cys Ile Lys Asn Gly Val			
10	150	155	160	165
	atc gtc aag cgc gcc atc ctc aac gac att agc gag gcc aag aag ctg			584
	Ile Val Lys Arg Ala Ile Leu Asn Asp Ile Ser Glu Ala Lys Lys Leu			
	170	175	180	
15	agc cac gcg ggc aag acg ccc aat atc atc gtc aac gcc acg ggt ctc			632
	Ser His Ala Gly Lys Thr Pro Asn Ile Ile Val Asn Ala Thr Gly Leu			
	185	190	195	
	ggc tcc tac aag ctg ggc ggt gtc gag gac aag acc atg gcg cct gcg			680
20	Gly Ser Tyr Lys Leu Gly Gly Val Glu Asp Lys Thr Met Ala Pro Ala			
	200	205	210	
	cgg gga cag att gtg gtt gtg cgc aac gag agc agc ccc atg ctc ctc			728
	Arg Gly Gln Ile Val Val Val Arg Asn Glu Ser Ser Pro Met Leu Leu			
25	215	220	225	
	act tca ggt gtc gag gac ggc ggt gct gat gtc atg tac ttg atg cag			776
	Thr Ser Gly Val Glu Asp Gly Gly Ala Asp Val Met Tyr Leu Met Gln			
30	230	235	240	245
	cga gca gct ggc ggt ggc acc atc ctg ggc ggt acc tac gac gtt ggc			824
	Arg Ala Ala Gly Gly Gly Thr Ile Leu Gly Gly Thr Tyr Asp Val Gly			
	250	255	260	
35	aac tgg gag tct cag cca gac ccc aac atc gcg aat cgc atc atg cag			872
	Asn Trp Glu Ser Gln Pro Asp Pro Asn Ile Ala Asn Arg Ile Met Gln			
	265	270	275	
	cgc atc gtc gag gtg cgg ccc gag att gcc aac ggc aag ggc gtc aag			920
40	Arg Ile Val Glu Val Arg Pro Glu Ile Ala Asn Gly Lys Gly Val Lys			
	280	285	290	
	ggg ctg agc gtg atc cga cac gcc gtc ggc atg cgg ccg tgg cga aag			968
	Gly Leu Ser Val Ile Arg His Ala Val Gly Met Arg Pro Trp Arg Lys			
45	295	300	305	

gac gga gtc agg atc gag gag gag aag ctg gat gat gag act tgg atc 1016
 Asp Gly Val Arg Ile Glu Glu Glu Lys Leu Asp Asp Glu Thr Trp Ile
 310 315 320 325
 5
 gtg cac aac tac gga cac tct gga tgg ggt tac cag ggt tcg tat ggt 1064
 Val His Asn Tyr Gly His Ser Gly Trp Gly Tyr Gln Gly Ser Tyr Gly
 330 335 340
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 tgt gct gag aat gta gtc cag ttg gtt gac aag gtc ggc aag gcg gcc 1112
 Cys Ala Glu Asn Val Val Gln Leu Val Asp Lys Val Gly Lys Ala Ala
 345 350 355
 aag tct aag ctg tagttgaaaa ggctgaatg agtaatagta attggatatt 1164
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 Lys Ser Lys Leu
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 ggaaataaccg tatttgccct cg 1186
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 <211> 361
 <212> PRT
 <213> Nectria haematococca
 25
 <400> 6
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 20 25 30
 Ala Lys His Met Pro Gly Asp Tyr Asp Val Glu Tyr Ala Ser Pro Phe
 35 40 45
 35
 Ala Gly Ala Asn His Ser Pro Met Ala Thr Glu Glu Ser Ser Glu Trp
 50 55 60
 Glu Arg Arg Thr Trp Tyr Glu Phe Lys Arg Leu Val Glu Glu Val Pro
 65 70 75 80
 40
 Glu Ala Gly Val His Phe Gln Lys Ser Arg Ile Gln Arg Arg Asn Val
 85 90 95
 Asp Thr Glu Lys Ala Gln Arg Ser Gly Phe Pro Asp Ala Leu Phe Ser
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 100 105 110

Lys Glu Pro Trp Phe Lys Asn Met Phe Glu Asp Phe Arg Glu Gln His
 115 120 125

5 Pro Ser Glu Val Ile Pro Gly Tyr Asp Ser Gly Cys Glu Phe Thr Ser
 130 135 140

Val Cys Ile Asn Thr Ala Ile Tyr Leu Pro Trp Leu Leu Gly Gln Cys
 145 150 155 160

10 Ile Lys Asn Gly Val Ile Val Lys Arg Ala Ile Leu Asn Asp Ile Ser
 165 170 175

Glu Ala Lys Lys Leu Ser His Ala Gly Lys Thr Pro Asn Ile Ile Val
 15 180 185 190

Asn Ala Thr Gly Leu Gly Ser Tyr Lys Leu Gly Gly Val Glu Asp Lys
 195 200 205

20 Thr Met Ala Pro Ala Arg Gly Gln Ile Val Val Val Arg Asn Glu Ser
 210 215 220

Ser Pro Met Leu Leu Thr Ser Gly Val Glu Asp Gly Gly Ala Asp Val
 225 230 235 240

25 Met Tyr Leu Met Gln Arg Ala Ala Gly Gly Gly Thr Ile Leu Gly Gly
 245 250 255

Thr Tyr Asp Val Gly Asn Trp Glu Ser Gln Pro Asp Pro Asn Ile Ala
 30 260 265 270

Asn Arg Ile Met Gln Arg Ile Val Glu Val Arg Pro Glu Ile Ala Asn
 275 280 285

35 Gly Lys Gly Val Lys Gly Leu Ser Val Ile Arg His Ala Val Gly Met
 290 295 300

Arg Pro Trp Arg Lys Asp Gly Val Arg Ile Glu Glu Glu Lys Leu Asp
 40 305 310 315 320

Asp Glu Thr Trp Ile Val His Asn Tyr Gly His Ser Gly Trp Gly Tyr
 325 330 335

45

Gln Gly Ser Tyr Gly Cys Ala Glu Asn Val Val Gln Leu Val Asp Lys
 340 345 350

Val Gly Lys Ala Ala Lys Ser Lys Leu
 5 355 360

<210> 7

<211> 1071

<212> DNA

10 <213> *Trigonopsis variabilis*

<220>

<221> CDS

<222> (1)..(1068)

15 <223>

<400> 7

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 Met Ala Lys Ile Val Val Ile Gly Ala Gly Val Ala Gly Leu Thr Thr
 20 1 5 10 15

gct ctt caa ctt ctt cgt aaa gga cat gag gtt aca att gtg tcc gag 96
 Ala Leu Gln Leu Leu Arg Lys Gly His Glu Val Thr Ile Val Ser Glu
 20 25 30

25 ttt acg ccc ggt gat ctt agt atc gga tat acc tcg cct tgg gca ggt 144
 Phe Thr Pro Gly Asp Leu Ser Ile Gly Tyr Thr Ser Pro Trp Ala Gly
 35 40 45

30 gcc aac tgg ctc aca ttt tac gat gga ggc aag tta gcc gac tac gat 192
 Ala Asn Trp Leu Thr Phe Tyr Asp Gly Gly Lys Leu Ala Asp Tyr Asp
 50 55 60

35 gcc gtc tct tat cct atc ttg cga gag ctg gct cga agc agc ccc gag 240
 Ala Val Ser Tyr Pro Ile Leu Arg Glu Leu Ala Arg Ser Ser Pro Glu
 65 70 75 80

40 gct gga att cga ctc atc agc caa cgc tcc cat gtt ctc aag cgt gat 288
 Ala Gly Ile Arg Leu Ile Ser Gln Arg Ser His Val Leu Lys Arg Asp
 85 90 95

ctt cct aaa ctg gaa gtt gcc atg tcg gcc atc tgt caa cgc aat ccc 336
 Leu Pro Lys Leu Glu Val Ala Met Ser Ala Ile Cys Gln Arg Asn Pro
 100 105 110

45

	tgg ttc aaa aac aca gtc gat tct ttc gag att atc gag gac agg tcc	384
	Trp Phe Lys Asn Thr Val Asp Ser Phe Glu Ile Ile Glu Asp Arg Ser	
	115 120 125	
5	agg att gtc cac gat gat gtg gct tat cta gtc gaa ttt cgt tcc gtt	432
	Arg Ile Val His Asp Asp Val Ala Tyr Leu Val Glu Phe Arg Ser Val	
	130 135 140	
10	tgt atc cac acc gga gtc tac ttg aac tgg ctg atg tcc caa tgc tta	480
	Cys Ile His Thr Gly Val Tyr Leu Asn Trp Leu Met Ser Gln Cys Leu	
	145 150 155 160	
15	tcg ctc ggc gcc acg gtg gtt aaa cgt cga gtg aac cat atc aag gat	528
	Ser Leu Gly Ala Thr Val Val Lys Arg Arg Val Asn His Ile Lys Asp	
	165 170 175	
20	gcc aat tta cta cac tcc tca gga tca cgc ccc gac gtg att gtc aac	576
	Ala Asn Leu Leu His Ser Ser Gly Ser Arg Pro Asp Val Ile Val Asn	
	180 185 190	
25	tgt agt ggt ctc ttt gcc cgg ttc ttg gga ggc gtc gag gac aag aag	624
	Cys Ser Gly Leu Phe Ala Arg Phe Leu Gly Gly Val Glu Asp Lys Lys	
	195 200 205	
30	atg tac cct att cga gga caa gtc gtc ctt gtt cga aac tct ctt cct	672
	Met Tyr Pro Ile Arg Gly Gln Val Val Leu Val Arg Asn Ser Leu Pro	
	210 215 220	
35	ttt atg gcc tcc ttt tcc agc act cct gaa aaa gaa aat gaa gac gaa	720
	Phe Met Ala Ser Phe Ser Ser Thr Pro Glu Lys Glu Asn Glu Asp Glu	
	225 230 235 240	
40	gct cta tat atc atg acc cga ttc gat ggt act tct atc att ggc ggt	768
	Ala Leu Tyr Ile Met Thr Arg Phe Asp Gly Thr Ser Ile Ile Gly Gly	
	245 250 255	
45	tgt ttc caa ccc aac aac tgg tca tcc gaa ccc gat cct tct ctc acc	816
	Cys Phe Gln Pro Asn Asn Trp Ser Ser Glu Pro Asp Pro Ser Leu Thr	
	260 265 270	
50	cat cga atc ctg tct aga gcc ctc gac cga ttc ccg gaa ctg acc aaa	864
	His Arg Ile Leu Ser Arg Ala Leu Asp Arg Phe Pro Glu Leu Thr Lys	
	275 280 285	

gat ggc cct ctt gac att gtg cgc gaa tgc gtt ggc cac cgt cct ggt 912
 Asp Gly Pro Leu Asp Ile Val Arg Glu Cys Val Gly His Arg Pro Gly
 290 295 300

5 aga gag ggc ggt ccc cga gta gaa tta gag aag atc ccc ggc gtt ggc 960
 Arg Glu Gly Gly Pro Arg Val Glu Leu Glu Lys Ile Pro Gly Val Gly
 305 310 315 320

10 ttt gtt gtc cat aac tat ggt gcc gcc ggt gct ggt tac caa tcc tct 1008
 Phe Val Val His Asn Tyr Gly Ala Ala Gly Ala Gly Tyr Gln Ser Ser
 325 330 335

15 tac ggc atg gct gat gaa gct gtt tct tac gtc gaa aga gct ctt act 1056
 Tyr Gly Met Ala Asp Glu Ala Val Ser Tyr Val Glu Arg Ala Leu Thr
 340 345 350

cgt cca aac ctt tag 1071
 Arg Pro Asn Leu
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<210> 8
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 <212> PRT

25 <213> Trigonopsis variabilis

<400> 8
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30 Ala Leu Gln Leu Leu Arg Lys Gly His Glu Val Thr Ile Val Ser Glu
 20 25 30

35 Phe Thr Pro Gly Asp Leu Ser Ile Gly Tyr Thr Ser Pro Trp Ala Gly
 35 40 45

Ala Asn Trp Leu Thr Phe Tyr Asp Gly Gly Lys Leu Ala Asp Tyr Asp
 50 55 60

40 Ala Val Ser Tyr Pro Ile Leu Arg Glu Leu Ala Arg Ser Ser Pro Glu
 65 70 75 80

Ala Gly Ile Arg Leu Ile Ser Gln Arg Ser His Val Leu Lys Arg Asp
 85 90 95

45

Leu Pro Lys Leu Glu Val Ala Met Ser Ala Ile Cys Gln Arg Asn Pro
 100 105 110

5 Trp Phe Lys Asn Thr Val Asp Ser Phe Glu Ile Ile Glu Asp Arg Ser
 115 120 125

Arg Ile Val His Asp Asp Val Ala Tyr Leu Val Glu Phe Arg Ser Val
 130 135 140

10 Cys Ile His Thr Gly Val Tyr Leu Asn Trp Leu Met Ser Gln Cys Leu
 145 150 155 160

Ser Leu Gly Ala Thr Val Val Lys Arg Arg Val Asn His Ile Lys Asp
 165 170 175

15 Ala Asn Leu Leu His Ser Ser Gly Ser Arg Pro Asp Val Ile Val Asn
 180 185 190

Cys Ser Gly Leu Phe Ala Arg Phe Leu Gly Gly Val Glu Asp Lys Lys
 20 195 200 205

Met Tyr Pro Ile Arg Gly Gln Val Val Leu Val Arg Asn Ser Leu Pro
 210 215 220

25 Phe Met Ala Ser Phe Ser Ser Thr Pro Glu Lys Glu Asn Glu Asp Glu
 225 230 235 240

Ala Leu Tyr Ile Met Thr Arg Phe Asp Gly Thr Ser Ile Ile Gly Gly
 245 250 255

30 Cys Phe Gln Pro Asn Asn Trp Ser Ser Glu Pro Asp Pro Ser Leu Thr
 260 265 270

His Arg Ile Leu Ser Arg Ala Leu Asp Arg Phe Pro Glu Leu Thr Lys
 35 275 280 285

Asp Gly Pro Leu Asp Ile Val Arg Glu Cys Val Gly His Arg Pro Gly
 290 295 300

40 Arg Glu Gly Gly Pro Arg Val Glu Leu Glu Lys Ile Pro Gly Val Gly
 305 310 315 320

Phe Val Val His Asn Tyr Gly Ala Ala Gly Ala Gly Tyr Gln Ser Ser
 325 330 335

45

Tyr Gly Met Ala Asp Glu Ala Val Ser Tyr Val Glu Arg Ala Leu Thr
 340 345 350

Arg Pro Asn Leu
 5 355

<210> 9

<211> 1047

10 <212> DNA

<213> Schizosaccharomyces pombe

<220>

<221> CDS

15 <222> (22)..(1041)

<223> coding for DAAO

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 Arg Asp Ile Val Ile Val Gly Ala Gly Val
 1 5 10

25 att gga ttg acc act gct tgg att ctt tca gac ttg ggt ctt gct cct 99
 Ile Gly Leu Thr Thr Ala Trp Ile Leu Ser Asp Leu Gly Leu Ala Pro
 15 20 25

30 cgt att aag gtg att gcc aag tat acg cct gaa gat cgt tct gta gaa 147
 Arg Ile Lys Val Ile Ala Lys Tyr Thr Pro Glu Asp Arg Ser Val Glu
 30 35 40

35 tac act tcc cct tgg gct ggc gca aat ttc tgt agc att tct gct act 195
 Tyr Thr Ser Pro Trp Ala Gly Ala Asn Phe Cys Ser Ile Ser Ala Thr
 45 50 55

40 gat gac aat gct ttg cgc tgg gat aaa atc act tac cat cgt ttc gcc 243
 Asp Asp Asn Ala Leu Arg Trp Asp Lys Ile Thr Tyr His Arg Phe Ala
 60 65 70

45 tac ttg gcg aaa act cgt cct gaa gca gga atc cgt ttt gct gat ctt 291
 Tyr Leu Ala Lys Thr Arg Pro Glu Ala Gly Ile Arg Phe Ala Asp Leu
 75 80 85 90

45 cga gaa ttg tgg gag tac gag ccg aaa cac gac aaa atc aga tcc tgg 339
 Arg Glu Leu Trp Glu Tyr Glu Pro Lys His Asp Lys Ile Arg Ser Trp
 95 100 105

	aat acc tat gtc aga gat ttc aaa gtt atc cct gaa aaa gat ctt cca	387
	Asn Thr Tyr Val Arg Asp Phe Lys Val Ile Pro Glu Lys Asp Leu Pro	
	110 115 120	
5	gga gaa tgt atc tac gga cat aag gcc acc acc ttt tta atc aac gct	435
	Gly Glu Cys Ile Tyr Gly His Lys Ala Thr Thr Phe Leu Ile Asn Ala	
	125 130 135	
10	cct cat tac ttg aat tat atg tac aag ctg ctc att gaa gct ggc gtc	483
	Pro His Tyr Leu Asn Tyr Met Tyr Lys Leu Leu Ile Glu Ala Gly Val	
	140 145 150	
15	gaa ttt gaa aag aaa gaa ttg agt cac atc aaa gag act gtc gaa gaa	531
	Glu Phe Glu Lys Lys Glu Leu Ser His Ile Lys Glu Thr Val Glu Glu	
	155 160 165 170	
20	act cca gaa gct tca gta gta ttt aat tgc act ggt ctc tgg gct tcc	579
	Thr Pro Glu Ala Ser Val Val Phe Asn Cys Thr Gly Leu Trp Ala Ser	
	175 180 185	
25	aaa ttg ggt ggc gtt gaa gac ccg gac gtt tat ccg act cgt gga cat	627
	Lys Leu Gly Gly Val Glu Asp Pro Asp Val Tyr Pro Thr Arg Gly His	
	190 195 200	
30	ggt gtt ttg gtt aag gct cct cat gta aca gaa act cgc att ttg aat	675
	Val Val Leu Val Lys Ala Pro His Val Thr Glu Thr Arg Ile Leu Asn	
	205 210 215	
35	ggc aag aac tct gat acc tat att att cct cgt ccc tta aat ggt gga	723
	Gly Lys Asn Ser Asp Thr Tyr Ile Ile Pro Arg Pro Leu Asn Gly Gly	
	220 225 230	
40	gtc att tgc ggc ggt ttc atg caa cca gga aac tgg gat cgt gaa att	771
	Val Ile Cys Gly Gly Phe Met Gln Pro Gly Asn Trp Asp Arg Glu Ile	
	235 240 245 250	
45	cac cct gaa gac act ttg gat atc ctt aag aga aca tcg gct ttg atg	819
	His Pro Glu Asp Thr Leu Asp Ile Leu Lys Arg Thr Ser Ala Leu Met	
	255 260 265	
50	cca gaa ttg ttc cac ggc aag ggt ccg gag ggt gct gaa att att caa	867
	Pro Glu Leu Phe His Gly Lys Gly Pro Glu Gly Ala Glu Ile Ile Gln	
	270 275 280	

gaa tgt gtc gga ttc cgt cct tct cga aag ggt ggt gcc cgc gta gag 915
 Glu Cys Val Gly Phe Arg Pro Ser Arg Lys Gly Gly Ala Arg Val Glu
 285 290 295

5 ctt gat gtt gtt ccc ggc acc tca gtc ccc ctt gtt cat gat tac ggt 963
 Leu Asp Val Val Pro Gly Thr Ser Val Pro Leu Val His Asp Tyr Gly
 300 305 310

10 gct tct ggc aca gga tac caa gct ggt tat ggt atg gct ctt gac tct 1011
 Ala Ser Gly Thr Gly Tyr Gln Ala Gly Tyr Gly Met Ala Leu Asp Ser
 315 320 325 330

gtc atg ttg gct ctt cct aaa atc aaa ttg gcttag 1047
 Val Met Leu Ala Leu Pro Lys Ile Lys Leu
 15 335 340

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 <211> 340
 20 <212> PRT
 <213> Schizosaccharomyces pombe

<400> 10
 Arg Asp Ile Val Ile Val Gly Ala Gly Val Ile Gly Leu Thr Thr Ala
 25 1 5 10 15

Trp Ile Leu Ser Asp Leu Gly Leu Ala Pro Arg Ile Lys Val Ile Ala
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30 Lys Tyr Thr Pro Glu Asp Arg Ser Val Glu Tyr Thr Ser Pro Trp Ala
 35 40 45

Gly Ala Asn Phe Cys Ser Ile Ser Ala Thr Asp Asp Asn Ala Leu Arg
 50 55 60

35 Trp Asp Lys Ile Thr Tyr His Arg Phe Ala Tyr Leu Ala Lys Thr Arg
 65 70 75 80

Pro Glu Ala Gly Ile Arg Phe Ala Asp Leu Arg Glu Leu Trp Glu Tyr
 40 85 90 95

Glu Pro Lys His Asp Lys Ile Arg Ser Trp Asn Thr Tyr Val Arg Asp
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 <212> DNA
 <213> Streptomyces coelicolor

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 <222> (31)..(957)
 <223> coding for DAAO

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<220>
 <221> misc_feature
 <222> (880)..(936)
 <223> DAAO signature

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 Gly Glu Val Val Val Val Gly Gly
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20

ggg gtg atc ggg ctg acg acg gcc gtc gtc ctc gcc gag cgg ggc aga 102
 Gly Val Ile Gly Leu Thr Thr Ala Val Val Leu Ala Glu Arg Gly Arg
 10 15 20

25

cgg gtg cgg ctg tgg acc cgg gag ccc gcg gag cgg acc acc tcg gtg 150
 Arg Val Arg Leu Trp Thr Arg Glu Pro Ala Glu Arg Thr Thr Ser Val
 25 30 35 40

30

gta gcg ggc ggg ctg tgg tgg ccg tac cgg atc gag ccg gtc gcg ctg 198
 Val Ala Gly Gly Leu Trp Trp Pro Tyr Arg Ile Glu Pro Val Ala Leu
 45 50 55

35

gcc cag gcc tgg gcg ctg cgt tcc ctg gac gtg tac gag gag ctg gcg 246
 Ala Gln Ala Trp Ala Leu Arg Ser Leu Asp Val Tyr Glu Glu Leu Ala
 60 65 70

40

gca cgg ccc ggg cag acc ggc gta cgc atg ctc gaa ggg gtg ctc ggc 294
 Ala Arg Pro Gly Gln Thr Gly Val Arg Met Leu Glu Gly Val Leu Gly
 75 80 85

gag acc ggc ctg gac gag gtg gac ggg tgg gcc gcg gcc cgg ctg ccg 342
 Glu Thr Gly Leu Asp Glu Val Asp Gly Trp Ala Ala Ala Arg Leu Pro
 90 95 100

45

ggg ctg cgc gcg gcg agc gcc gcc gag tac gcc ggg acg ggg ctg tgg 390

	Gly	Leu	Arg	Ala	Ala	Ser	Ala	Ala	Glu	Tyr	Ala	Gly	Thr	Gly	Leu	Trp	
	105					110					115					120	
5	gcg	cgg	ctg	cgg	ctc	atc	gac	atg	tcg	acc	cat	ctg	cgg	tgg	ctg	cgg	438
	Ala	Arg	Leu	Pro	Leu	Ile	Asp	Met	Ser	Thr	His	Leu	Pro	Trp	Leu	Arg	
					125					130					135		
10	gag	cgg	ctg	ctg	gcc	gcg	ggc	ggc	acg	gtg	gag	gac	cgc	gcg	gtg	acc	486
	Glu	Arg	Leu	Leu	Ala	Ala	Gly	Gly	Thr	Val	Glu	Asp	Arg	Ala	Val	Thr	
					140					145					150		
15	gat	ctg	gcc	gag	gcg	gac	gcg	cgg	gtg	gtg	gtc	aac	tgc	acc	ggc	ctg	534
	Asp	Leu	Ala	Glu	Ala	Asp	Ala	Pro	Val	Val	Val	Asn	Cys	Thr	Gly	Leu	
					155					160					165		
	ggc	gcc	cgg	gag	ctg	gtg	cgg	gac	cgg	gcg	gta	cgg	cgg	gtg	cgc	gga	582
	Gly	Ala	Arg	Glu	Leu	Val	Pro	Asp	Pro	Ala	Val	Arg	Pro	Val	Arg	Gly	
					170					175					180		
20	cag	ctg	gtc	gtc	gtg	gag	aac	ccc	ggc	atc	cac	aac	tgg	ctg	gtc	gcg	630
	Gln	Leu	Val	Val	Val	Glu	Asn	Pro	Gly	Ile	His	Asn	Trp	Leu	Val	Ala	
	185						190				195					200	
25	gcc	gac	gcg	gac	tcc	ggg	gag	acg	acg	tac	ttc	ctt	cgg	cag	cgg	gga	678
	Ala	Asp	Ala	Asp	Ser	Gly	Glu	Thr	Thr	Tyr	Phe	Leu	Pro	Gln	Pro	Gly	
					205					210					215		
30	cgg	ctc	ctg	ctg	ggc	ggc	acg	gct	gag	gag	gac	gcc	tgg	tcg	acc	gag	726
	Arg	Leu	Leu	Leu	Gly	Gly	Thr	Ala	Glu	Glu	Asp	Ala	Trp	Ser	Thr	Glu	
					220					225					230		
35	cgg	gac	cgg	gag	gtc	gcg	gcg	gcc	atc	gtg	cga	cgg	tgc	gcg	gcc	ctg	774
	Pro	Asp	Pro	Glu	Val	Ala	Ala	Ala	Ile	Val	Arg	Arg	Cys	Ala	Ala	Leu	
					235					240					245		
	cgt	ccc	gag	atc	gcc	gga	gcg	cgg	gtg	ctc	gcg	cac	ctg	gtg	ggg	ctg	822
	Arg	Pro	Glu	Ile	Ala	Gly	Ala	Arg	Val	Leu	Ala	His	Leu	Val	Gly	Leu	
					250					255					260		
40	cgg	cgg	gcc	cgg	gac	gcg	gtc	cgg	ctg	gag	cgc	ggg	acg	ctg	cgg	gac	870
	Arg	Pro	Ala	Arg	Asp	Ala	Val	Arg	Leu	Glu	Arg	Gly	Thr	Leu	Pro	Asp	
	265						270				275					280	
45	ggg	cgc	cgg	ctg	gtg	cac	aac	tac	ggt	cac	ggc	ggc	gcg	ggc	gtc	acc	918
	Gly	Arg	Arg	Leu	Val	His	Asn	Tyr	Gly	His	Gly	Gly	Ala	Gly	Val	Thr	

	285	290	295	
	gtg gcc tgg ggc tgc gct cag gag gcg gcc cgg ctc gcc tcctga			963
	Val Ala Trp Gly Cys Ala Gln Glu Ala Ala Arg Leu Ala			
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	<223> DAAO signature			
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25	Pro Ala Glu Arg Thr Thr Ser Val Val Ala Gly Gly Leu Trp Trp Pro			
	35	40	45	
	Tyr Arg Ile Glu Pro Val Ala Leu Ala Gln Ala Trp Ala Leu Arg Ser			
	50	55	60	
30	Leu Asp Val Tyr Glu Glu Leu Ala Ala Arg Pro Gly Gln Thr Gly Val			
	65	70	75	80
	Arg Met Leu Glu Gly Val Leu Gly Glu Thr Gly Leu Asp Glu Val Asp			
35	85	90	95	
	Gly Trp Ala Ala Ala Arg Leu Pro Gly Leu Arg Ala Ala Ser Ala Ala			
	100	105	110	
40	Glu Tyr Ala Gly Thr Gly Leu Trp Ala Arg Leu Pro Leu Ile Asp Met			
	115	120	125	
	Ser Thr His Leu Pro Trp Leu Arg Glu Arg Leu Leu Ala Ala Gly Gly			
	130	135	140	
45				

Thr Val Glu Asp Arg Ala Val Thr Asp Leu Ala Glu Ala Asp Ala Pro
 145 150 155 160

5 Val Val Val Asn Cys Thr Gly Leu Gly Ala Arg Glu Leu Val Pro Asp
 165 170 175

Pro Ala Val Arg Pro Val Arg Gly Gln Leu Val Val Val Glu Asn Pro
 180 185 190

10 Gly Ile His Asn Trp Leu Val Ala Ala Asp Ala Asp Ser Gly Glu Thr
 195 200 205

Thr Tyr Phe Leu Pro Gln Pro Gly Arg Leu Leu Leu Gly Gly Thr Ala
 210 215 220

15 Glu Glu Asp Ala Trp Ser Thr Glu Pro Asp Pro Glu Val Ala Ala Ala
 225 230 235 240

Ile Val Arg Arg Cys Ala Ala Leu Arg Pro Glu Ile Ala Gly Ala Arg
 20 245 250 255

Val Leu Ala His Leu Val Gly Leu Arg Pro Ala Arg Asp Ala Val Arg
 260 265 270

25 Leu Glu Arg Gly Thr Leu Pro Asp Gly Arg Arg Leu Val His Asn Tyr
 275 280 285

Gly His Gly Gly Ala Gly Val Thr Val Ala Trp Gly Cys Ala Gln Glu
 290 295 300

30 Ala Ala Arg Leu Ala
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35 <210> 13
 <211> 1038
 <212> DNA
 <213> Candida boidinii

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 <223> coding for DAO

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act aca tac tgt tta atc tat gag gct gga tgt gct cca gct aaa att 96
Thr Thr Tyr Cys Leu Ile Tyr Glu Ala Gly Cys Ala Pro Ala Lys Ile
20 25 30

10 act att gtt gct gaa ttt tta cca ggt gat caa tct aca tta tat aca 144
Thr Ile Val Ala Glu Phe Leu Pro Gly Asp Gln Ser Thr Leu Tyr Thr
35 . 40 45

15 tct cca tgg gca ggt ggt aat ttt tct tgt att tca cca gct gat gat 192
Ser Pro Trp Ala Gly Gly Asn Phe Ser Cys Ile Ser Pro Ala Asp Asp
 50 55 60

aca aca ttg gct tat gat aaa ttc aca tat ctt aat tta ttc aag att . 240
Thr Thr Leu Ala Tyr Asp Lys Phe Thr Tyr Leu Asn Leu Phe Lys Ile
20 65 70 75 80

cac aaa aaa tta ggt gga cca gaa tgt gga tta gat aat aag cca agt 288
His Lys Lys Leu Gly Gly Pro Glu Cys Gly Leu Asp Asn Lys Pro Ser
 85 90 95

act gaa tat tgg gat ttt tat cct ggt gat gaa aaa gtc aat tct tta 336
Thr Glu Tyr Trp Asp Phe Tyr Pro Gly Asp Glu Lys Val Asn Ser Leu
100 105 110

30 aaa caa tat ctt aaa gat ttt aaa gtt att cca aaa tca gaa tta cca 384
Lys Gln Tyr Leu Lys Asp Phe Lys Val Ile Pro Lys Ser Glu Leu Pro
 115 120 125

35 gaa ggt gtt gaa tat ggt att agt tat act aca tgg aat ttc aac tgt 432
Glu Gly Val Glu Tyr Gly Ile Ser Tyr Thr Thr Trp Asn Phe Asn Cys
 130 135 140

cct gtt ttc tta caa aat atg gct aat ttt tta aat aaa aga aat gtt 480
 Pro Val Phe Leu Gln Asn Met Ala Asn Phe Leu Asn Lys Arg Asn Val
 40 145 150 155 160

acc att att aga aaa cat tta aca cat att tct caa gct tat tta aca 528
Thr Ile Ile Arg Lys His Leu Thr His Ile Ser Gln Ala Tyr Leu Thr
165 170 175

45

	gtt aat aca aaa gtt gtt ttc aac tgt aca ggt att ggt gct gct gat	576
	Val Asn Thr Lys Val Val Phe Asn Cys Thr Gly Ile Gly Ala Ala Asp	
	180 185 190	
5	tta ggt ggt gtt aaa gat gaa aaa gtt tat cca act aga gga caa gtt	624
	Ieu Gly Gly Val Lys Asp Glu Lys Val Tyr Pro Thr Arg Gly Gln Val	
	195 200 205	
10	gtt gtt gtt aga gct cca cat att caa gaa aat aaa atg aga tgg ggt	672
	Val Val Val Arg Ala Pro His Ile Gln Glu Asn Lys Met Arg Trp Gly	
	210 215 220	
15	aaa gac tat gct act tat att att cca aga cca tat tct aat ggt gaa	720
	Lys Asp Tyr Ala Thr Tyr Ile Ile Pro Arg Pro Tyr Ser Asn Gly Glu	
	225 230 235 240	
20	tta gtc tta ggt ggt ttc tta caa aag gat aat tgg aca ggt aat act	768
	Leu Val Leu Gly Gly Phe Leu Gln Lys Asp Asn Trp Thr Gly Asn Thr	
	245 250 255	
	ttt ggt ttt gaa act gat gat att gtt agt aga act aca tct tta tta	816
	Phe Gly Phe Glu Thr Asp Asp Ile Val Ser Arg Thr Thr Ser Leu Leu	
	260 265 270	
25	cca aag att tta gat gaa cca ctt cat att att aga gtt gca gct ggt	864
	Pro Lys Ile Leu Asp Glu Pro Leu His Ile Ile Arg Val Ala Ala Gly	
	275 280 285	
30	tta aga cca agt aga cat ggt ggt cca aga att gaa gct gaa gtt tgt	912
	Leu Arg Pro Ser Arg His Gly Gly Pro Arg Ile Glu Ala Glu Val Cys	
	290 295 300	
35	gaa gaa ggt aaa tta act att cat aat tat ggt gct tct gga tat ggt	960
	Glu Glu Gly Lys Leu Thr Ile His Asn Tyr Gly Ala Ser Gly Tyr Gly	
	305 310 315 320	
40	tat caa gct ggt tat ggt atg tct tat gaa gct gtc aaa ctt tta gtt	1008
	Tyr Gln Ala Gly Tyr Gly Met Ser Tyr Glu Ala Val Lys Leu Leu Val	
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	gat aac caa aaa gtt aaa gct aaa ctt tag	1038
	Asp Asn Gln Lys Val Lys Ala Lys Leu	
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<210> 14
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 <212> PRT
 <213> Candida boidinii

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10 Thr Thr Tyr Cys Leu Ile Tyr Glu Ala Gly Cys Ala Pro Ala Lys Ile
 20 25 30

Thr Ile Val Ala Glu Phe Leu Pro Gly Asp Gln Ser Thr Leu Tyr Thr
 35 40 45

15

Ser Pro Trp Ala Gly Gly Asn Phe Ser Cys Ile Ser Pro Ala Asp Asp
 50 55 60

20 Thr Thr Leu Ala Tyr Asp Lys Phe Thr Tyr Leu Asn Leu Phe Lys Ile
 65 70 75 80

His Lys Lys Leu Gly Gly Pro Glu Cys Gly Leu Asp Asn Lys Pro Ser
 85 90 95

25 Thr Glu Tyr Trp Asp Phe Tyr Pro Gly Asp Glu Lys Val Asn Ser Leu
 100 105 110

Lys Gln Tyr Leu Lys Asp Phe Lys Val Ile Pro Lys Ser Glu Leu Pro
 115 120 125

30

Glu Gly Val Glu Tyr Gly Ile Ser Tyr Thr Thr Trp Asn Phe Asn Cys
 130 135 140

35 Pro Val Phe Leu Gln Asn Met Ala Asn Phe Leu Asn Lys Arg Asn Val
 145 150 155 160

Thr Ile Ile Arg Lys His Leu Thr His Ile Ser Gln Ala Tyr Leu Thr
 165 170 175

40 Val Asn Thr Lys Val Val Phe Asn Cys Thr Gly Ile Gly Ala Ala Asp
 180 185 190

Leu Gly Gly Val Lys Asp Glu Lys Val Tyr Pro Thr Arg Gly Gln Val
 195 200 205

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Val Val Val Arg Ala Pro His Ile Gln Glu Asn Lys Met Arg Trp Gly
 210 215 220

5 Lys Asp Tyr Ala Thr Tyr Ile Ile Pro Arg Pro Tyr Ser Asn Gly Glu
 225 230 235 240

10 Leu Val Leu Gly Gly Phe Leu Gln Lys Asp Asn Trp Thr Gly Asn Thr
 245 250 255

Phe Gly Phe Glu Thr Asp Asp Ile Val Ser Arg Thr Thr Ser Leu Leu
 260 265 270

15 Pro Lys Ile Leu Asp Glu Pro Leu His Ile Ile Arg Val Ala Ala Gly
 275 280 285

Leu Arg Pro Ser Arg His Gly Gly Pro Arg Ile Glu Ala Glu Val Cys
 290 295 300

20 Glu Glu Gly Lys Leu Thr Ile His Asn Tyr Gly Ala Ser Gly Tyr Gly
 305 310 315 320

Tyr Gln Ala Gly Tyr Gly Met Ser Tyr Glu Ala Val Lys Leu Leu Val
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 <222> (38)..(183)
 <223> Agrobacterium right border

40 <220>
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 <222> (445)..(462)
 <223> recognition / cleavage site for I-SceI endonuclease

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<223> complementary: 35S terminator
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<223> complementary: coding for pTOP10P tetracyclin regulatable promoter
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<223> complementary: coding for Rhodotorula gracilis D-amino acid oxidase
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30 <223> complementary: Arabidopsis thaliana nitrilase I promoter
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35 <223> complementary: OCS terminator
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40 <223> complementary: coding for tetracyclin repressor rtTA
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45 <223> complementary: coding for Pisum sativum ptxA promoter

<220>

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<222> (7345)..(7549)

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<223> complementary: coding for 23S terminator (functioning as homology sequence)

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<222> (7618)..(7834)

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<223> Agrobacterium left border

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	atcagatctg	gtaccgcgtc	actggatttt	ggtttttagg	attagaaatt	ttattgatag	240
	aagtatttta	caaatacaaa	tacatactaa	gggtttctta	tatgctcaac	acatgagcga	300
	aaccctataa	gaacccta	tcccttatct	gggaactact	cacacattat	tctggagaaa	360
	aatagagaga	gatagatttg	tagagagaga	ctggtgattt	ttgcgcgggg	taccccaaac	420
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